

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph on page 29 beginning with line 22 with the following amended paragraph:

Additional illustrative embodiments of the invention disclosed herein include 84P2A9-related proteins containing the amino acid residues of one or more of the biological motifs contained within the 84P2A9-related protein sequence as shown in Figure 2. In one embodiment, proteins of the invention comprise one or more of the 84P2A9 nuclear localization sequences such as RKRR (SEQ ID NO: 449) at residues 42-50 of SEQ ID NO: 2, RKRR (SEQ ID NO: 449) at residues 47-50 of SEQ ID NO: 2, KRRP (SEQ ID NO: 450) at residues 101-104 of SEQ ID NO: 2, RRRRRK (SEQ ID NO: 451) at residues 135-139 of SEQ ID NO: 2 and/or KKRRK (SEQ ID NO: 452) at residues 186-189 of SEQ ID NO: 2. In another embodiment, proteins of the invention comprise one or more of the 84P2A9 N-glycosylation sites such as NRTL (SEQ ID NO: 453) at residues 131-134 of SEQ ID NO: 2, NQTN (SEQ ID NO: 454) at residues 212-215 of SEQ ID NO: 2 and/or NCSV (SEQ ID NO: 455) at residues 394-397 of SEQ ID NO: 2. In another embodiment, proteins of the invention comprise one or more of the regions of 84P2A9 that exhibit homology to LUCA 15 and/or KIAA1152. In another embodiment, proteins of the invention comprise one or more of the 84P2A9 cAMP and cGMP-dependent protein kinase phosphorylation sites such as KRRS (SEQ ID NO: 456) at residues 48-51 of SEQ ID NO: 2 and/or RRPS (SEQ ID NO: 457) at residues 102-105 of SEQ ID NO: 2. In another embodiment, proteins of the invention comprise one or more of the 84P2A9 Protein Kinase C phosphorylation sites such as TLR (SEQ ID NO: 458) at residues 133-135 of SEQ ID NO: 2, SNK (SEQ ID NO: 459) at residues 152-154 of SEQ ID NO: 2, SDR (SEQ ID NO: 460) at residues 171-173 of SEQ ID NO: 2, TNK (SEQ ID NO: 461) at residues 214-216 of SEQ ID NO: 2, SRR (SEQ ID NO: 462) at residues 313-315 of SEQ ID NO: 2, SSK (SEQ ID NO: 463) at residues 328-330 of SEQ ID NO: 2 and/or SVR (SEQ ID NO: 464) at residues 396-398 of SEQ ID NO: 2. In another embodiment, proteins of the invention comprise one or more of the 84P2A9 casein kinase II phosphorylation sites such as SALE (SEQ ID NO: 465) at residues 10-

13 of SEQ ID NO: 2, SSLE (SEQ ID NO: 466) at residues 70-73 of SEQ ID NO: 2, SLEE (SEQ ID NO: 467) at residues 71-74 of SEQ ID NO: 2, SDSD (SEQ ID NO: 468) at residues 91-94 of SEQ ID NO: 2, TNKD (SEQ ID NO: 469) at residues 214-217 of SEQ ID NO: 2, SESD (SEQ ID NO: 470) at residues 232-235 of SEQ ID NO: 2, SSTD (SEQ ID NO: 471) at residues 240-243 of SEQ ID NO: 2, TNDE (SEQ ID NO: 472) at residues 248-251 of SEQ ID NO: 2, TELD (SEQ ID NO: 473) at residues 287-290 of SEQ ID NO: 2 and/or TEHD (SEQ ID NO: 474) at residues 374-377 of SEQ ID NO: 2. In another embodiment, proteins of the invention comprise one or more of the N-myristoylation sites such as GSDSSL (SEQ ID NO: 475) at residues 67-72 of SEQ ID NO: 2, GLFTND (SEQ ID NO: 476) at residues 245-250 of SEQ ID NO: 2, GGACGI (SEQ ID NO: 477) at residues 269-274 of SEQ ID NO: 2, GGTPTS (SEQ ID NO: 478) at residues 336-341 of SEQ ID NO: 2, GTPTSM (SEQ ID NO: 479) at residues 337-342 of SEQ ID NO: 2, GSLCTG (SEQ ID NO: 480) at residues 409-414 of SEQ ID NO: 2, GSGLGR (SEQ ID NO: 481) at residues 459-464 of SEQ ID NO: 2 and/or at residues 481-486 of SEQ ID NO: 2. In another embodiment, proteins of the invention comprise one or more amidation sites such as RGRK (SEQ ID NO: 483) at residues 45-48 of SEQ ID NO: 2 and/or RGKR (SEQ ID NO: 484) at residues 113-116 of SEQ ID NO: 2. An illustrative embodiment of such a polypeptide includes two or more amino acid sequences selected from the group consisting of KKRK (SEQ ID NO: 452), NQTN (SEQ ID NO: 454), NCSV (SEQ ID NO: 455), TNK (SEQ ID NO: 461), SRR (SEQ ID NO: 462), SSK (SEQ ID NO: 463), SVR (SEQ ID NO: 464), GLFTND (SEQ ID NO: 476), GGACGI (SEQ ID NO: 477), GGTPTS (SEQ ID NO: 478), GTPTSM (SEQ ID NO: 479) and GSLCTG (SEQ ID NO: 480) (as identified above in SEQ ID NO: 2). In a preferred embodiment, the polypeptide comprises three or four or five or six or more amino acid sequences KKRK (SEQ ID NO: 452), NQTN (SEQ ID NO: 454), NCSV (SEQ ID NO: 455), TNK (SEQ ID NO: 461), SRR (SEQ ID NO: 462), SSK (SEQ ID NO: 463), SVR (SEQ ID NO: 464), GLFTND (SEQ ID NO: 476), GGACGI (SEQ ID NO: 477), GGTPTS (SEQ ID NO: 478), GTPTSM (SEQ ID NO: 479) and GSLCTG (SEQ ID NO: 480) (as identified above in SEQ ID NO: 2).

Please replace Table 3A on page 88 with the following amended table:

Table 3A - HLA Peptide Scoring Results - 84P2A9 - A1 9-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
1.	71	(SEQ ID NO: 29)	SLEEPSKDY	45.000
2.	469	(SEQ ID NO: 30)	ISEPIQAMQ	27.000
3.	283	(SEQ ID NO: 31)	KEDPTELDK	25.000
4.	15	(SEQ ID NO: 32)	SSEQARGGF	13.500
5.	23	(SEQ ID NO: 33)	FAETGDHSR	9.000
6.	441	(SEQ ID NO: 34)	ILENNIGNR	9.000
7.	241	(SEQ ID NO: 35)	STDAGLFTN	6.250
8.	72	(SEQ ID NO: 36)	LEEPSKDYL	4.500
9.	233	(SEQ ID NO: 37)	ESDSSSLSS	3.750
10.	92	(SEQ ID NO: 38)	DSDDQMLVA	3.750
11.	157	(SEQ ID NO: 39)	MTQPPEGCR	2.500
12.	413	(SEQ ID NO: 40)	TGDIKRRRK	2.500
13.	256	(SEQ ID NO: 41)	DDEQSDWFY	2.250
14.	373	(SEQ ID NO: 42)	RTEHDQHQL	2.250
15.	309	(SEQ ID NO: 43)	MSHPSRRGF	1.500
16.	207	(SEQ ID NO: 44)	ESEETNQTN	1.350
17.	231	(SEQ ID NO: 45)	MSEDSSSL	1.350
18.	64	(SEQ ID NO: 46)	LSEGSDSSL	1.350
19.	456	(SEQ ID NO: 47)	WTPGSGLGR	1.250
20.	375	(SEQ ID NO: 48)	EHDQHQLLR	1.250
21.	293	(SEQ ID NO: 49)	VPDPVFESI	1.250
22.	93	(SEQ ID NO: 50)	SDDQMLVAK	1.000
23.	494	(SEQ ID NO: 51)	ATTPNAGK	1.000
24.	208	(SEQ ID NO: 52)	SEETNQTNK	0.900
25.	205	(SEQ ID NO: 53)	VLESEETNQ	0.900
26.	79	(SEQ ID NO: 54)	YRENNNNK	0.900
27.	11	(SEQ ID NO: 55)	ALESSEQA	0.900
28.	226	(SEQ ID NO: 56)	VSELMSES	0.750
29.	31	(SEQ ID NO: 57)	RSISCPLKR	0.750
30.	90	(SEQ ID NO: 58)	HSDSDDQML	0.750

Please replace Table 4A on page 91 with the following amended table:

Table 4A - HLA Peptide Scoring Results - 84P2A9 - A1 10-mers	
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine	

Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
1.	469	(SEQ ID NO: 59)	ISEPIQAMQR	675.000
2.	92	(SEQ ID NO: 60)	DSDDQMLVAK	30.000
3.	207	(SEQ ID NO: 61)	ESEETNQTNK	27.000
4.	168	(SEQ ID NO: 62)	DMDSDRAYQY	25.000
5.	11	(SEQ ID NO: 63)	ALEESSEQAR	9.000
6.	71	(SEQ ID NO: 64)	SLEEPSKDYR	9.000
7.	282	(SEQ ID NO: 65)	EKEDPTELDK	4.500
8.	166	(SEQ ID NO: 66)	DQDMDSDRAY	3.750
9.	90	(SEQ ID NO: 67)	HSDSDDQMLV	3.570
10.	177	(SEQ ID NO: 68)	YQEFTKNKVK	2.700
11.	144	(SEQ ID NO: 69)	AVDLPQDISN	2.500
12.	373	(SEQ ID NO: 70)	RTEHDQHQLL	2.250
13.	33	(SEQ ID NO: 71)	ISCPLKRQAR	1.500
14.	231	(SEQ ID NO: 72)	MSESDSSSLs	1.350
15.	15	(SEQ ID NO: 73)	SSEQARGGFA	1.350
16.	254	(SEQ ID NO: 74)	QGDDEQSDWF	1.250
17.	255	(SEQ ID NO: 75)	GDDEQSDWFY	1.250
18.	293	(SEQ ID NO: 76)	VPDPVFESIL	1.250
19.	173	(SEQ ID NO: 77)	RAYQYQEFTK	1.000
20.	481	(SEQ ID NO: 78)	GLGLGFPLPK	1.000
21.	205	(SEQ ID NO: 79)	VLESEETNQT	0.900
22.	79	(SEQ ID NO: 80)	YREHNHNNKK	0.900
23.	441	(SEQ ID NO: 81)	ILENNIGNRM	0.900
24.	23	(SEQ ID NO: 82)	FAETGDHSRS	0.900
25.	121	(SEQ ID NO: 83)	ESDFAVDNVG	0.750
26.	233	(SEQ ID NO: 84)	ESDSSSLsST	0.750
27.	409	(SEQ ID NO: 85)	GSLCTGDIKR	0.750
28.	259	(SEQ ID NO: 86)	QSDWFYEKES	0.750
29.	70	(SEQ ID NO: 87)	SSLEEPSKDY	0.750
30.	67	(SEQ ID NO: 88)	GSDSSLEEPS	0.750

Please replace Table 5A on page 94 with the following amended table:

Table 5A - HLA Peptide Scoring Results - 84P2A9 - A2 9-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
1.	300	(SEQ ID NO: 89)	SILTGSFPL	63.035
2.	449	(SEQ ID NO: 90)	RMLQNMGWT	32.748
3.	4	(SEQ ID NO: 91)	LVHDLVSAL	29.965
4.	238	(SEQ ID NO: 92)	SLSSTDAGL	21.362
5.	198	(SEQ ID NO: 93)	KIQDEGVVL	17.282

Table 5A - HLA Peptide Scoring Results - 84P2A9 - A2 9-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
6.	433	(SEQ ID NO: 94)	FVGENAQPI	17.217
7.	301	(SEQ ID NO: 95)	ILTGSFPLM	16.047
8.	218	(SEQ ID NO: 96)	KMECEEQKV	11.252
9.	480	(SEQ ID NO: 97)	KGLGLGFPL	10.474
10.	461	(SEQ ID NO: 98)	GLGRDGKGI	10.433
11.	341	(SEQ ID NO: 99)	SMVPIPGPV	6.530
12.	468	(SEQ ID NO: 100)	GISEPIQAM	6.442
13.	405	(SEQ ID NO: 101)	SMHLGSLCT	5.382
14.	191	(SEQ ID NO: 102)	KIIRQGPKI	5.021
15.	117	(SEQ ID NO: 103)	PLWHESDFA	2.445
16.	177	(SEQ ID NO: 104)	YQEFTKNKV	2.076
17.	454	(SEQ ID NO: 105)	MGWTPGSGL	1.968
18.	156	(SEQ ID NO: 106)	TMTQPPEGC	1.758
19.	374	(SEQ ID NO: 107)	TEHDQHQLL	1.703
20.	52	(SEQ ID NO: 108)	YNVHHPWET	1.678
21.	474	(SEQ ID NO: 109)	QAMQRPKGL	1.098
22.	240	(SEQ ID NO: 110)	SSTDAGLFT	1.097
23.	438	(SEQ ID NO: 111)	AQPILENNI	1.058
24.	269	(SEQ ID NO: 112)	GGACGITGV	1.044
25.	143	(SEQ ID NO: 113)	MAVDLPQDI	1.010
26.	206	(SEQ ID NO: 114)	LESEETNQT	1.010
27.	173	(SEQ ID NO: 115)	RAYQYQEFT	0.893
28.	3	(SEQ ID NO: 116)	ELVHDLVSA	0.857
29.	132	(SEQ ID NO: 117)	RTLRRRRKV	0.715
30.	266	(SEQ ID NO: 118)	KESGGACGI	0.710

Please replace Table 6A on page 97 with the following amended table:

Table 6A - HLA Peptide Scoring Results - 84P2A9 - A2 10-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
1.	230	(SEQ ID NO: 119)	LMSES DSSSL	107.536
2.	63	(SEQ ID NO: 120)	CLSEGSDSSL	87.586
3.	117	(SEQ ID NO: 121)	PLWHESDFAV	73.661
4.	453	(SEQ ID NO: 122)	NMGWTPGSGL	15.428
5.	475	(SEQ ID NO: 123)	AMQRPKGLGL	15.428
6.	433	(SEQ ID NO: 124)	FVGENAQPII	14.454
7.	323	(SEQ ID NO: 125)	RLHGMSSKNI	10.433

Table 6A - HLA Peptide Scoring Results - 84P2A9 - A2 10-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
8.	142	(SEQ ID NO: 126)	RMAVDLPQDI	7.535
9.	483	(SEQ ID NO: 127)	GLGFPLPKST	7.452
10.	300	(SEQ ID NO: 128)	SILTGSFPLM	4.802
11.	3	(SEQ ID NO: 129)	ELVHDLVSAL	3.685
12.	473	(SEQ ID NO: 130)	IQAMQRPKGL	3.682
13.	292	(SEQ ID NO: 131)	NVPDPVFESI	3.485
14.	124	(SEQ ID NO: 132)	FAVDNVGNRT	1.952
15.	334	(SEQ ID NO: 133)	KSGGTPTSMV	1.589
16.	445	(SEQ ID NO: 134)	NIGNRMLQNM	1.571
17.	315	(SEQ ID NO: 135)	RGFQARLSRL	1.187
18.	268	(SEQ ID NO: 136)	SGGACGITGV	1.044
19.	288	(SEQ ID NO: 137)	ELDKNVDPDV	1.022
20.	486	(SEQ ID NO: 138)	FPLPKSTSAT	0.828
21.	205	(SEQ ID NO: 139)	VLESEETNQT	0.811
22.	402	(SEQ ID NO: 140)	RQTSMHLGSL	0.648
23.	425	(SEQ ID NO: 141)	LPGPTTAGFV	0.552
24.	441	(SEQ ID NO: 142)	ILENNIGNRM	0.541
25.	237	(SEQ ID NO: 143)	SSLSSTDAGL	0.516
26.	10	(SEQ ID NO: 144)	SALEESSEQA	0.513
27.	212	(SEQ ID NO: 145)	NQTNKDKMEC	0.504
28.	301	(SEQ ID NO: 146)	ILTGSFPLMS	0.481
29.	239	(SEQ ID NO: 147)	LSSTDAGLFT	0.455
30.	103	(SEQ ID NO: 148)	RPSSNLNNNV	0.454

Please replace Table 7A on page 100 with the following amended table:

Table 7A - HLA Peptide Scoring Results - 84P2A9 - A3 9-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
1.	326	(SEQ ID NO: 149)	GMSSKNIKK	120.000
2.	245	(SEQ ID NO: 150)	GLFTNDEGR	60.000
3.	133	(SEQ ID NO: 151)	TLRRRRKVK	10.000
4.	146	(SEQ ID NO: 152)	DLPQDISNK	9.000
5.	410	(SEQ ID NO: 153)	SLCTGDIKR	8.000
6.	107	(SEQ ID NO: 154)	NLNNNVRGK	6.000
7.	258	(SEQ ID NO: 155)	EQSDWFYEK	4.860
8.	71	(SEQ ID NO: 156)	SLEEPSKDY	4.500
9.	381	(SEQ ID NO: 157)	LLRDNRAER	4.000

Table 7A - HLA Peptide Scoring Results - 84P2A9 - A3 9-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
10.	441	(SEQ ID NO: 158)	ILENNIGNR	1.800
11.	494	(SEQ ID NO: 159)	ATTPNAGK	1.500
12.	301	(SEQ ID NO: 160)	ILTGSFPLM	0.900
13.	461	(SEQ ID NO: 161)	GLGRDGKGI	0.900
14.	128	(SEQ ID NO: 162)	NVGNRTLRR	0.800
15.	238	(SEQ ID NO: 163)	SLSSTDAGL	0.600
16.	307	(SEQ ID NO: 164)	PLMSHPSRR	0.600
17.	456	(SEQ ID NO: 165)	WTPGSGLGR	0.600
18.	218	(SEQ ID NO: 166)	KMECEEQKV	0.600
19.	283	(SEQ ID NO: 167)	KEDPTELDK	0.540
20.	409	(SEQ ID NO: 168)	GSLCTGDIK	0.450
21.	273	(SEQ ID NO: 169)	GITGVVPWW	0.405
22.	344	(SEQ ID NO: 170)	PIPGVGNK	0.405
23.	184	(SEQ ID NO: 171)	KVKKRKLKI	0.360
24.	156	(SEQ ID NO: 172)	TMTQPPEGC	0.300
25.	11	(SEQ ID NO: 173)	ALEESSEQA	0.300
26.	180	(SEQ ID NO: 174)	FTKNKVKKR	0.300
27.	35	(SEQ ID NO: 175)	CPLKRQARK	0.300
28.	459	(SEQ ID NO: 176)	GSGLGRDGK	0.300
29.	191	(SEQ ID NO: 177)	KIIRQGPKI	0.270
30.	483	(SEQ ID NO: 178)	GLGFPLPKS	0.270

Please replace Table 8A on page 103 with the following amended table:

Table 8A - HLA Peptide Scoring Results - 84P2A9 - A3 10-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
1.	481	(SEQ ID NO: 179)	GLGLGFPLPK	360.000
2.	189	(SEQ ID NO: 180)	KLKIIRQGPK	18.000
3.	71	(SEQ ID NO: 181)	SLEEPSKDYR	6.000
4.	11	(SEQ ID NO: 182)	ALEESSEQAR	6.000
5.	380	(SEQ ID NO: 183)	QLLRDNRAER	6.000
6.	175	(SEQ ID NO: 184)	YQYQEFTKNK	4.500
7.	274	(SEQ ID NO: 185)	ITGVVPWWEK	4.500
8.	133	(SEQ ID NO: 186)	TLRRRRKVKR	4.000
9.	168	(SEQ ID NO: 187)	DMDSDRAYQY	3.600
10.	173	(SEQ ID NO: 188)	RAYYQEFTK	3.000
11.	410	(SEQ ID NO: 189)	SLCTGDIKRR	3.000

Table 8A - HLA Peptide Scoring Results - 84P2A9 - A3 10-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
12.	156	(SEQ ID NO: 190)	TMTQPPEGCR	1.800
13.	146	(SEQ ID NO: 191)	DLPQDISNKR	1.800
14.	107	(SEQ ID NO: 192)	NLNNNVRGKR	1.800
15.	475	(SEQ ID NO: 193)	AMQRPKGLGL	1.200
16.	63	(SEQ ID NO: 194)	CLSEGSDSSL	0.900
17.	453	(SEQ ID NO: 195)	NMGWTPGSGL	0.900
18.	230	(SEQ ID NO: 196)	LMSEDSSSL	0.900
19.	3	(SEQ ID NO: 197)	ELVHDLVSAL	0.810
20.	132	(SEQ ID NO: 198)	RTLRRRRKVK	0.750
21.	180	(SEQ ID NO: 199)	FTKNKVKRK	0.750
22.	343	(SEQ ID NO: 200)	VPIPGPVGNK	0.608
23.	238	(SEQ ID NO: 201)	SLSSTDAGLF	0.600
24.	142	(SEQ ID NO: 202)	RMAVDLPQDI	0.600
25.	257	(SEQ ID NO: 203)	DEQSDWFYEK	0.486
26.	323	(SEQ ID NO: 204)	RLHGMSSKNI	0.450
27.	301	(SEQ ID NO: 205)	ILTGSFPLMS	0.360
28.	117	(SEQ ID NO: 206)	PLWHESDFAV	0.300
29.	493	(SEQ ID NO: 207)	SATTPNAGK	0.300
30.	177	(SEQ ID NO: 208)	YQEFTKNKVK	0.300

Please replace Table 9A on page 106 with the following amended table:

Table 9A - HLA Peptide Scoring Results - 84P2A9 - A11 9-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
1.	326	(SEQ ID NO: 209)	GMSSKNIKK	2.400
2.	174	(SEQ ID NO: 210)	AYQYQEFTK	1.200
3.	494	(SEQ ID NO: 211)	ATTPNAGK	1.000
4.	128	(SEQ ID NO: 212)	NVGNRTLRR	0.800
5.	245	(SEQ ID NO: 213)	GLFTNDEGR	0.480
6.	456	(SEQ ID NO: 214)	WTPGSLGR	0.400
7.	258	(SEQ ID NO: 215)	EQSDWFYEK	0.360
8.	283	(SEQ ID NO: 216)	KEDPTELDK	0.360
9.	35	(SEQ ID NO: 217)	CPLKRQARK	0.300
10.	133	(SEQ ID NO: 218)	TLRRRRKVK	0.200
11.	176	(SEQ ID NO: 219)	QYQEFTKNK	0.200
12.	157	(SEQ ID NO: 220)	MTQPPEGCR	0.200
13.	40	(SEQ ID NO: 221)	QARKRRGRK	0.200

Table 9A - HLA Peptide Scoring Results - 84P2A9 - A11 9-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
14.	80	(SEQ ID NO: 222)	RENHNNNKK	0.180
15.	410	(SEQ ID NO: 223)	SLCTGDIKR	0.160
16.	210	(SEQ ID NO: 224)	ETNQTNKDK	0.150
17.	146	(SEQ ID NO: 225)	DLPQDISNK	0.120
18.	184	(SEQ ID NO: 226)	KVKKRKLKI	0.120
19.	180	(SEQ ID NO: 227)	FTKNKVKKR	0.100
20.	409	(SEQ ID NO: 228)	GSLCTGDIK	0.090
21.	381	(SEQ ID NO: 229)	LLRDNRAER	0.080
22.	441	(SEQ ID NO: 230)	ILENNIGNR	0.080
23.	482	(SEQ ID NO: 231)	LGLGFPLPK	0.060
24.	459	(SEQ ID NO: 232)	GSGLGRDGK	0.060
25.	275	(SEQ ID NO: 233)	TGVVPWWEK	0.060
26.	139	(SEQ ID NO: 234)	KVKRMAVDL	0.060
27.	208	(SEQ ID NO: 235)	SEETNQTNK	0.060
28.	306	(SEQ ID NO: 236)	FPLMSHPSR	0.060
29.	178	(SEQ ID NO: 237)	QEFTKNKVK	0.060
30.	179	(SEQ ID NO: 238)	EFTKNKVKK	0.060

Please replace Table 10A on page 109 with the following amended table:

Table 10A - HLA Peptide Scoring Results - 84P2A9 - A11 10-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
1.	173	(SEQ ID NO: 239)	RAYQYQEFTK	3.600
2.	481	(SEQ ID NO: 240)	GLGLGFPLPK	2.400
3.	132	(SEQ ID NO: 241)	RTLRRRRKVK	2.250
4.	274	(SEQ ID NO: 242)	ITGVVPWWEK	2.000
5.	39	(SEQ ID NO: 243)	RQARKRRGRK	1.800
6.	189	(SEQ ID NO: 244)	KLKIIRQGPK	1.200
7.	175	(SEQ ID NO: 245)	YQYQEFTKNK	0.600
8.	180	(SEQ ID NO: 246)	FTKNKVKKRK	0.500
9.	177	(SEQ ID NO: 247)	YQEFTKNKVK	0.300
10.	343	(SEQ ID NO: 248)	VPIPGPVGNK	0.300
11.	493	(SEQ ID NO: 249)	SATTPNAGK	0.200
12.	34	(SEQ ID NO: 250)	SCPLKRQARK	0.200
13.	178	(SEQ ID NO: 251)	QEFTKNKVKK	0.120
14.	78	(SEQ ID NO: 252)	DYRENHNNNK	0.120
15.	380	(SEQ ID NO: 253)	QLLRDNRAER	0.120

Table 10A - HLA Peptide Scoring Results - 84P2A9 - A11 10-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
16.	22	(SEQ ID NO: 254)	GFAETGDHSR	0.120
17.	412	(SEQ ID NO: 255)	CTGDIKRRRK	0.100
18.	133	(SEQ ID NO: 256)	TLRRRRKVKR	0.080
19.	71	(SEQ ID NO: 257)	SLEEPSKDYR	0.080
20.	325	(SEQ ID NO: 258)	HGMSSKNIKK	0.080
21.	107	(SEQ ID NO: 259)	NLNNNVRGKR	0.080
22.	11	(SEQ ID NO: 260)	ALEESSEQAR	0.080
23.	156	(SEQ ID NO: 261)	TMTQPPEGCR	0.080
24.	182	(SEQ ID NO: 262)	KNKVKKRKLK	0.060
25.	216	(SEQ ID NO: 263)	KDKMECEEQK	0.060
26.	383	(SEQ ID NO: 264)	RDNRAERGHK	0.060
27.	306	(SEQ ID NO: 265)	FPLMSHPSRR	0.060
28.	128	(SEQ ID NO: 266)	NVGNRTLRRR	0.040
29.	111	(SEQ ID NO: 267)	NVRGKRPLWH	0.040
30.	311	(SEQ ID NO: 268)	HPSRRGFQAR	0.040

Please replace Table 11A on page 112 with the following amended table:

Table 11A - HLA Peptide Scoring Results - 84P2A9 - A1 10-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
1.	316	(SEQ ID NO: 269)	GFQARLSRL	30.000
2.	480	(SEQ ID NO: 270)	KGLGLGFPL	14.400
3.	198	(SEQ ID NO: 271)	KIQDEGVVL	14.400
4.	373	(SEQ ID NO: 272)	RTEHDQHQL	12.000
5.	182	(SEQ ID NO: 273)	KNKVKKRKKL	8.800
6.	139	(SEQ ID NO: 274)	KVKRMAVDL	8.000
7.	263	(SEQ ID NO: 275)	FYEKESGGA	7.500
8.	78	(SEQ ID NO: 276)	DYRENHNNN	7.200
9.	300	(SEQ ID NO: 277)	SILTGSPFL	6.000
10.	474	(SEQ ID NO: 278)	QAMQRPKGL	6.000
11.	116	(SEQ ID NO: 279)	RPLWHESDF	6.000
12.	110	(SEQ ID NO: 280)	NNVRGKRPL	6.000
13.	231	(SEQ ID NO: 281)	MSESDSSSL	6.000
14.	434	(SEQ ID NO: 282)	VGENAQFIL	6.000
15.	64	(SEQ ID NO: 283)	LSEGSDSSL	6.000
16.	443	(SEQ ID NO: 284)	ENNIGNRML	6.000
17.	4	(SEQ ID NO: 285)	LVHDLVSAL	5.760

Table 11A - HLA Peptide Scoring Results - 84P2A9 - A1 10-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
18.	29	(SEQ ID NO: 286)	HSRSISCPL	5.600
19.	56	(SEQ ID NO: 287)	HPWETGHCL	4.800
20.	90	(SEQ ID NO: 288)	HSDSDDQML	4.800
21.	478	(SEQ ID NO: 289)	RPKGLGLGF	4.800
22.	476	(SEQ ID NO: 290)	MQRPKGLGL	4.800
23.	400	(SEQ ID NO: 291)	ASRQTSMHL	4.000
24.	454	(SEQ ID NO: 292)	MGWTPGSGL	4.000
25.	238	(SEQ ID NO: 293)	SLSSTDAGL	4.000
26.	403	(SEQ ID NO: 294)	QTSMHLGSL	4.000
27.	191	(SEQ ID NO: 295)	KIIRQGPKI	3.300
28.	349	(SEQ ID NO: 296)	VGNKRMVHF	3.000
29.	15	(SEQ ID NO: 297)	SSEQARGGF	3.000
30.	143	(SEQ ID NO: 298)	MAVDLPQDI	2.592

Please replace Table 12A on page 115 with the following amended table:

Table 12A - HLA Peptide Scoring Results - 84P2A9 - A24 10-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
1.	297	(SEQ ID NO: 299)	VFESILTGSF	18.000
2.	373	(SEQ ID NO: 300)	RTEHDQHQLL	14.400
3.	176	(SEQ ID NO: 301)	QYQEFTKNKV	11.880
4.	174	(SEQ ID NO: 302)	AYQYQEFTKN	9.900
5.	432	(SEQ ID NO: 303)	GFVGENAQPI	9.000
6.	51	(SEQ ID NO: 304)	SYNVHHPWET	8.250
7.	402	(SEQ ID NO: 305)	RQTSMHLGSL	8.000
8.	315	(SEQ ID NO: 306)	RGFQARLSRL	8.000
9.	263	(SEQ ID NO: 307)	FYEKESGGAC	7.500
10.	3	(SEQ ID NO: 308)	ELVHDLVSAL	7.200
11.	280	(SEQ ID NO: 309)	WWEKEDPTL	6.600
12.	237	(SEQ ID NO: 310)	SSLSTDAGL	6.000
13.	299	(SEQ ID NO: 311)	ESILTGSFPL	6.000
14.	475	(SEQ ID NO: 312)	AMQRPKGLGL	6.000
15.	109	(SEQ ID NO: 313)	NNNVRGKRPL	6.000
16.	230	(SEQ ID NO: 314)	LMSEDSSSL	4.800
17.	293	(SEQ ID NO: 315)	VPDPVFESIL	4.800
18.	433	(SEQ ID NO: 316)	FVGENAQPIL	4.800
19.	63	(SEQ ID NO: 317)	CLSEGSDSSL	4.800

Table 12A - HLA Peptide Scoring Results - 84P2A9 - A24 10-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
20.	125	(SEQ ID NO: 318)	AVDNVGNRTL	4.000
21.	99	(SEQ ID NO: 319)	VAKRRPSSNL	4.000
22.	473	(SEQ ID NO: 320)	IQAMQRPKGL	4.000
23.	453	(SEQ ID NO: 321)	NMGWTPGSG	4.000
24.	399	(SEQ ID NO: 322)	TASRQTSML	4.000
25.	292	(SEQ ID NO: 323)	NVPDPVFESI	3.024
26.	142	(SEQ ID NO: 324)	RMAVDLPQDI	2.880
27.	437	(SEQ ID NO: 325)	NAQPILENNI	2.592
28.	254	(SEQ ID NO: 326)	QGDDEQSDWF	2.400
29.	14	(SEQ ID NO: 327)	ESSEQARGGF	2.400
30.	323	(SEQ ID NO: 328)	RLHGMSSKNI	2.000

Please replace Table 13A on page 118 with the following amended table:

Table 13A - HLA Peptide Scoring Results - 84P2A9 - B7 9-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
1.	400	(SEQ ID NO: 329)	ASRQTSML	120.000
2.	56	(SEQ ID NO: 330)	HPWETGHCL	80.000
3.	476	(SEQ ID NO: 331)	MQRPKGLGL	40.000
4.	29	(SEQ ID NO: 332)	HSRSISCPL	40.000
5.	474	(SEQ ID NO: 333)	QAMQRPKGL	36.000
6.	4	(SEQ ID NO: 334)	LVHDLVSAL	20.000
7.	139	(SEQ ID NO: 335)	KVKRMAVDL	20.000
8.	100	(SEQ ID NO: 336)	AKRRPSSNL	18.00
9.	423	(SEQ ID NO: 337)	APLPGPTTA	6.000
10.	454	(SEQ ID NO: 338)	MGWTPGSG	6.000
11.	396	(SEQ ID NO: 339)	SVRTASRQT	5.000
12.	196	(SEQ ID NO: 340)	GPKIQDEGV	4.000
13.	182	(SEQ ID NO: 341)	KNKVKKRKL	4.000
14.	110	(SEQ ID NO: 342)	NNVRGKRPL	4.000
15.	198	(SEQ ID NO: 343)	KIQDEGVVL	4.000
16.	403	(SEQ ID NO: 344)	QTSMLGSL	4.000
17.	238	(SEQ ID NO: 345)	SLSSTDAGL	4.000
18.	285	(SEQ ID NO: 346)	DPTELDKNV	4.000
19.	300	(SEQ ID NO: 347)	SILTGSFPL	4.000
20.	347	(SEQ ID NO: 348)	GPVGNKRMV	4.000
21.	480	(SEQ ID NO: 349)	KGLGLGFPL	4.000

Table 13A - HLA Peptide Scoring Results - 84P2A9 - B7 9-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
22.	417	(SEQ ID NO: 350)	KRRRKAAPL	4.000
23.	443	(SEQ ID NO: 351)	ENNIGNRML	4.000
24.	313	(SEQ ID NO: 352)	SRRGFQARL	4.000
25.	18	(SEQ ID NO: 353)	QARGGFAET	3.000
26.	293	(SEQ ID NO: 354)	VPDPVFESI	2.400
27.	295	(SEQ ID NO: 355)	DPVFESILT	2.000
28.	311	(SEQ ID NO: 356)	HPSRRGFQA	2.000
29.	433	(SEQ ID NO: 357)	FVGENAQPI	2.000
30.	486	(SEQ ID NO: 358)	FPLPKSTSA	2.000

Please replace Table 14A on page 121 with the following amended table:

Table 14A - HLA Peptide Scoring Results - 84P2A9 - B7 10-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
1.	318	(SEQ ID NO: 359)	QARLSRLHGM	30.000
2.	293	(SEQ ID NO: 360)	VPDPVFESIL	24.000
3.	345	(SEQ ID NO: 361)	IPGPVGNKRM	20.000
4.	433	(SEQ ID NO: 362)	FVGENAQPIL	20.000
5.	125	(SEQ ID NO: 363)	AVDENVGNRTL	18.000
6.	99	(SEQ ID NO: 364)	VAKRRPSSNL	18.000
7.	399	(SEQ ID NO: 365)	TASRQTSMHL	12.000
8.	475	(SEQ ID NO: 366)	AMQRPKGLGL	12.000
9.	453	(SEQ ID NO: 367)	NMGWTPGSGL	6.000
10.	230	(SEQ ID NO: 368)	LMSESDSSSL	4.000
11.	473	(SEQ ID NO: 369)	IQAMQRPKGL	4.000
12.	312	(SEQ ID NO: 370)	PSRRGFQARL	4.000
13.	425	(SEQ ID NO: 371)	LPGPTTAGFV	4.000
14.	103	(SEQ ID NO: 372)	RPSSNLNNNV	4.000
15.	109	(SEQ ID NO: 373)	NNNVRGKRPL	4.000
16.	63	(SEQ ID NO: 374)	CLSEGSDSSL	4.000
17.	315	(SEQ ID NO: 375)	RGFQARLSRL	4.000
18.	237	(SEQ ID NO: 376)	SSLSSTDAGL	4.000
19.	416	(SEQ ID NO: 377)	IKRRRKAAPL	4.000
20.	196	(SEQ ID NO: 378)	GPKIQDEGVV	4.000
21.	299	(SEQ ID NO: 379)	ESILTGSFPL	4.000
22.	402	(SEQ ID NO: 380)	RQTSMHLSL	4.000
23.	3	(SEQ ID NO: 381)	ELVHDLVSAL	4.000

Table 14A - HLA Peptide Scoring Results - 84P2A9 - B7 10-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
24.	147	(SEQ ID NO: 382)	LPQDISNKRT	2.000
25.	116	(SEQ ID NO: 383)	RPLWHESDFA	2.000
26.	278	(SEQ ID NO: 384)	VPWWEKEDPT	2.000
27.	488	(SEQ ID NO: 385)	LPKSTSATT	2.000
28.	292	(SEQ ID NO: 386)	NVPDPVFESI	2.000
29.	45	(SEQ ID NO: 387)	RGRKRRSYNV	2.000
30.	486	(SEQ ID NO: 388)	FPLPKSTSAT	2.000

Please replace Table 15A on page 124 with the following amended table:

Table 15A - HLA Peptide Scoring Results - 84P2A9 - B35 9-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
1.	478	(SEQ ID NO: 389)	RPKGLGLGF	120.000
2.	56	(SEQ ID NO: 390)	HPWETGHCL	40.000
3.	116	(SEQ ID NO: 391)	RPLWHESDF	40.000
4.	425	(SEQ ID NO: 392)	LPGPTTAGF	20.000
5.	334	(SEQ ID NO: 393)	KSGGTPTSM	20.000
6.	400	(SEQ ID NO: 394)	ASRQTSMHL	15.000
7.	29	(SEQ ID NO: 395)	HSRSISCPL	15.000
8.	196	(SEQ ID NO: 396)	GPKIQDEGV	12.000
9.	285	(SEQ ID NO: 397)	DPTELDKNV	8.000
10.	239	(SEQ ID NO: 398)	LSSTDAGLF	7.500
11.	139	(SEQ ID NO: 399)	KVKRMAVDL	6.000
12.	233	(SEQ ID NO: 400)	EQKVSDELM	6.000
13.	488	(SEQ ID NO: 401)	LPKSTSATT	6.000
14.	198	(SEQ ID NO: 402)	KIQDEGVVL	6.000
15.	182	(SEQ ID NO: 403)	KNKVKKRKL	6.000
16.	309	(SEQ ID NO: 404)	MSHPSRRGF	5.000
17.	360	(SEQ ID NO: 405)	DSHHHDHWF	5.000
18.	50	(SEQ ID NO: 406)	RSYNVHHPW	5.000
19.	103	(SEQ ID NO: 407)	RPSSNLNNN	4.000
20.	468	(SEQ ID NO: 408)	GISEPIQAM	4.000
21.	347	(SEQ ID NO: 409)	GPVGNKRMV	4.000
22.	398	(SEQ ID NO: 410)	RTASRQTSM	4.000
23.	295	(SEQ ID NO: 411)	DPVFESILT	3.000
24.	476	(SEQ ID NO: 412)	MQRPKGLGL	3.000
25.	74	(SEQ ID NO: 413)	EPSKDYREN	3.000

Table 15A - HLA Peptide Scoring Results - 84P2A9 - B35 9-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
26.	474	(SEQ ID NO: 414)	QAMQRPKGL	3.000
27.	143	(SEQ ID NO: 415)	MAVDLPQDI	2.400
28.	184	(SEQ ID NO: 416)	KVKKRKLKI	2.400
29.	293	(SEQ ID NO: 417)	VPDPVFESI	2.400
30.	90	(SEQ ID NO: 418)	HSDSDDQML	2.250

Please replace Table 16A on page 127 with the following amended table:

Table 16A - HLA Peptide Scoring Results - 84P2A9 - B35 10-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
1.	345	(SEQ ID NO: 419)	IPGPVGNKRM	40.000
2.	70	(SEQ ID NO: 420)	SSLEEPSKDY	20.000
3.	196	(SEQ ID NO: 421)	GPKIQDEGVV	18.000
4.	318	(SEQ ID NO: 422)	QARLSRLHGM	18.000
5.	14	(SEQ ID NO: 423)	ESSEQARGGF	10.000
6.	99	(SEQ ID NO: 424)	VAKRRPSSNL	9.000
7.	103	(SEQ ID NO: 425)	RPSSNLNNNV	8.000
8.	116	(SEQ ID NO: 426)	RPLWHESDFA	6.000
9.	488	(SEQ ID NO: 427)	LPKSTSATTT	6.000
10.	293	(SEQ ID NO: 428)	VPDPVFESIL	6.000
11.	299	(SEQ ID NO: 429)	ESILTGSFPL	5.000
12.	237	(SEQ ID NO: 430)	SSLSSTDAGL	5.000
13.	467	(SEQ ID NO: 431)	KGISEPIQAM	4.000
14.	56	(SEQ ID NO: 432)	HPWETGHCLS	4.000
15.	147	(SEQ ID NO: 433)	LPQDISNKRT	4.000
16.	425	(SEQ ID NO: 434)	LPGPTTAGFV	4.000
17.	358	(SEQ ID NO: 435)	SPDSHHHDHW	3.000
18.	230	(SEQ ID NO: 436)	LMSESDSSSL	3.000
19.	253	(SEQ ID NO: 437)	RQGDDEQSDW	3.000
20.	399	(SEQ ID NO: 438)	TASRQTSMHL	3.000
21.	184	(SEQ ID NO: 439)	KVKKRKLKII	2.400
22.	445	(SEQ ID NO: 440)	NIGNRMLQNM	2.000
23.	402	(SEQ ID NO: 441)	RQTSMHLGSL	2.000
24.	300	(SEQ ID NO: 442)	SILTGSFPLM	2.000
25.	334	(SEQ ID NO: 443)	KSGGTPTSMV	2.000
26.	433	(SEQ ID NO: 444)	FVGENAQPII	2.000
27.	210	(SEQ ID NO: 445)	ETNQTNKDKM	2.000

Table 16A - HLA Peptide Scoring Results - 84P2A9 - B35 10-mers				
Each peptide is a portion of SEQ ID NO: 2; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine				
Rank	Start Position	SEQ ID NO:	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of a Molecule Containing This Subsequence)
28.	63	(SEQ ID NO: 446)	CLSEGSDSSL	2.000
29.	486	(SEQ ID NO: 447)	FPLPKSTSAT	2.000
30.	315	(SEQ ID NO: 448)	RGFQARLSRL	2.000